

FIG. 1

1	CTCTAGATGTACATGGAGGATGACCGAAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA	60
1	M T E K T N G V K S S P A N	14
61	TAATCACAAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCAACAGGAC	120
15	N H N H H A P P A I K A N G K D D H R T	34
121	AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC	180
35	S S R P H S A A D D D T S S E L Q R L A	54
181	AGACGTGGATGCCACAGCAGGGAAAGGAGTGGCTTCCGCAGGATAGTTCGCCTGGTGG	240
55	D V D A P Q Q G R S G F R R I V R L V G	74
241	GATCATCAGAGAATGGCCAACAAGAATTCCGAGAGGAGGAACCTAGGCCTGACTCATT	300
75	I I R E W A N K N F R E E E P R P D S F	94
301	CCTCGAGCGTTTCTGGCCCTGAACCTCCAGACTGTGACCAACAGGAGGGGATGGCAA	360
95	L E R F R G P E L Q T V T T Q E G D G K	114
361	AGGCAGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTGAACTATTGTCTTGG	420
115	G D K D G E D K G T K K K F E L F V L D	134
421	CCCAGCTGGGGATTGTACTACTGCTGGCTATTGTCTATTGCCATGCCGTCTTACAA	480
135	P A G D L Y Y C W L F V I A M P V L Y N	154
481	CTGGTGCCTGCTGGCTGCCAGAGCCTGCTCAGTGACCTACAGAAAGGCTACTACCTGGT	540
155	W C L L V A R A C F S D L Q K G Y Y L V	174
541	GTGGCTGGTCTGGATTATGTCTCAGATGTGGTCTACATTGGACCTCTTCATCCGATT	600
175	W L V L D Y V S D V V Y I A D L F I R L	194
601	GCGCACAGGTTCTGGAGCAGGGCTGCTGGTCAAAGATACCAAGAAACTGCGAGACAA	660
195	R T G F L E Q G L L V K D T K K L R D N	214
661	CTACATCCACACCCTGCAGTTCAAGCTGGATGTGGCTCCATCCCCACTGACCTGAT	720
215	Y I H T L Q F K L D V A S I I P T D L I	234
721	CTATTTGCTGGACATCCACAGCCCTGAGGTGCGCTCAACGCCCTGCTGCACCTTGC	780
235	Y F A V D I H S P E V R F N R L L H F A	254
781	CCGCATGTTGAGTTCTTGACCGGACAGAGACACGCACCAACTACCTAACATCTCCG	840
255	R M F E F D R T E T R T N Y P N I F R	274
841	CATCAGCAACCTTGCTCTACATCTGGTCATCATCCACTGGAAATGCCATCTATT	900
275	I S N L V L Y I L V I I H W N A C I Y Y	294
901	TGCCATCTCCAAATCCATAGGCTTGGGTGACACCTGGTTACCAAACATCACTGA	960
295	A I S K S I G F G V D T W V Y P N I T D	314

FIG. 1 (Cont'd)

961	CCCTGAGTATGGCTACCTGGCTAGGGAAATACATCTATTGCCCTTACTGGTCCACACTGAC	1020
315	P E Y G Y L A R E Y I Y C L Y W S T L T	334
1021	TCTCACTACCATTGGGGAGACACCACCCCTGTAAGGATGAGGAGTACCTATTGTCAT	1080
335	L T T I G E T P P P V K D E E Y L F V I	354
1081	CTTGACTTCCTGATTGGCGCTCATCTTGCCACCATCGGGAAATGTGGCTCCAT	1140
355	F D F L I G V L I F A T I V G N V G S M	374
1141	GATCTCCAACATGAATGCCACCCGGGAGTTCCAGGCTAAAGATCGATGCCGTGAAACA	1200
375	I S N M N A T R A E F Q A K I D A V K H	394
1201	CTACATGCAGTTCCGAAAGGTCAAGCAAGGGATGGAAGCCAAGGTCAATTAGGTGGTTGA	1260
395	Y M Q F R K V S K G M E A K V I R W F D	414
1261	CTACTTGTGGACCAATAAGAAGACAGTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC	1320
415	Y L W T N K K T V D E R E I L K N L P A	434
1321	CAAGCTCAGGGCTGAGATAGCCACCAATGTCCACTTGTCCACACTCAAGAAAGTGCAGC	1380
435	K L R A E I A T N V H L S T L K K V R I	454
1381	CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCCCTCAGGT	1440
455	F H D C E A G L L V E L V L K L R P Q V	474
1441	CTTCAGTCCTGGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT	1500
475	F S P G D Y I C R K G D I G K E M Y I I	494
1501	TAAGGAGGGCAAACCTGGCAGTGGTGGCTGATGATGGTGTACTCAGTATGCTCTGCTGTC	1560
495	K E G K L A V V A D D G V T Q Y A L L S	514
1561	GGCTGGAAGCTGCTTGGCGAGATCAGTATCCTAACATTAAGGGCAGTAAATGGCAA	1620
515	A G S C F G E I S I L N I K G S K M G N	534
1621	TCGACGCACAGCTAATATCCGCAGCCTGGCTACTCAGATCTCTCTGCTTGTCCAAGGA	1680
535	R R T A N I R S L G Y S D L F C L S K D	554
1681	TGATCTTATGGAAGCTGTGACTGAGTACCCCTGATGCCAAGAAAGTCCTAGAAGAGAGGG	1740
555	D L M E A V T E Y P D A K K V L E E R G	574
1741	TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAACGAAAGTGGCAACCAGCATGGA	1800
575	R E I L M K E G L L D E N E V A T S M E	594
1801	GGTCGACGTGCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAAACCTTGTACACTCG	1860
595	V D V Q E K L G Q L E T N M E T L Y T R	614
1861	CTTTGGCCGCCTGCTGGCTGAGTACACGGGGGCCAGCAGAACGCTCAAGCAGCGCATCAC	1920
615	F G R L L A E Y T G A Q Q K L K Q R I T	634

FIG. 1 (Cont'd)

1921	AGTTCTGGAAACCAAGATGAAACAGAACATGAAGATGACTACCTGTCTGATGGGATGAA	1980
635	V L E T K M K Q N N E D D Y L S D G M N	654
1981	CAGCCCTGAGCTGGCTGCTGACGAGCCATAAAGACCTGGGGCCCAACTGCCTCTCCAG	2040
655	S P E L A A A D E P	664
2041	CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTAGATCTCCGGATTTACAT	2100
2101	GCATTACCCCTCATGTTCCCTGAATTCTCCAAAAGTCTCTGACCTGNGTTTGGCC	2160
2161	TAAACATCCAAGATTCCGCCTCGGAT	2186

FIG. 2

MTEKTNGVKSSPANNHHAPPAIKANGKDDHRTSSRPHSAADDTSSELQRLADVDAPQQGRSGFRRI
VRLVGIIREWANKNFREEEPRPDSFLERFRGPELQTVTQEGDGKGDKGEDKGTKKFELFVLDAGD
LYYCWLFWIAMPVLYNWCLLVARACFSQDLQKGYYLVWLVDYVSDVVIADLFIRLRTGFLEQGLLVKD
TKKLRLDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRLHARMFEFFDRTETRTNYPNIFRIS
NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTIGETPPP
KDEEYLFVIFDFLIGVLIFATIVGNVGMISNMNATRAEFQAKIDAVKHMQFRKVSKGMEAKVIRWFD
YLWTNKKTVDEREILKNLPAKLRAEIATNVHLSTLKKVRIHDCEAGLLVELVLKLRPQVSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGESISILNIKGSKMGNRTANIRSLGYSDLFCLS
KDDLMEAVTEYPDAAKKVLEERGREILMKEGLLDENEVATSMEVDVQEKLGOLETNMETLYTRFGRLLAE
YTGAQQKLKQRITVLETKMQNNEDDYLSDMNSPELAAADEP

FIG. 3

MTEKTNGVKSSPANNHHAPPAIKANGKDDHRTSSRPHSAADDTSSELQRLADVDAPQQGRSGFRRI
VRLVGIIREWANKNFREEEPRPDSFLERFRGPELQTVTTQEGDGKGDGEDKGTKKFELFVLDAGD
LYYCWLFIAMPVLYNWCLLVARACFSDLQKGYYL**VWLVDYVSDVVIADLFIRLRTGFLEQGLLVKD**
TKKLRDNYIHTLQFKLDVASIIPTDIYFAVDIHSPEVRFNRLLHFARMFEFFDRTERTNYPNIFRIS
NLVLYILVIIHNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLWSTLTTTIGETPPPV
KDEEYL**FVIFDFLIGVLIFATIVGNVGS**MSISNMNATRAEFQAKIDAVKH**YMQFRKVSKG**MEAKVIRWFD
YLWTNKKTVDEREILKNLPAKLRAE**IATNVHLSTLKKVR**IFHDCEAGLLVELVLKLRPQVFSPGDYICR
KGDIGKEMYI**IKEGK**LAVVADDGVTQYALLSAGSCFG**EISILNIKGSKMGNRTANIRSLG**YSDLFCCLS
KDDLM**EA**VT**EY**PD**AK**KV**LE**ERG**RE**ILM**KE**GL**D**EN**E**VA**T**SM**E**VD**V**Q**E**KL**G**Q**LE**T**N**ME**T**LY**TR**FG**R**LLAE
YTGAQQKL**K**QRITV**L**ET**K**M**K**QN**N**ED**D**Y**L**SD**G**M**N**SP**E**L**A**AD**E**P

FIG. 4

			1		50
HBMYCNG	(1)				
CNG2_BOS	(1)				
CNG2_MOUSE	(1)				
CNG2_RAT	(1)				
rACNG	(1)	MSSWRSCARAPLSGSAWRRSAATRRSRRCLTKRKRWSSGKTPMQSTQC			
			51		100
HBMYCNG	(1)	MTEKNGVKSSPANNHNHHAPPAIKANGKDDH			
CNG2_BOS	(1)	MTEKANGVKSSPANNHNHHAPPAIKASGKDDH			
CNG2_MOUSE	(1)	MMTEKSNGVKSSPANNHNHHPPPSIKANGKDDH			
CNG2_RAT	(1)	MMTEKSNGVKSSPANNHNHHPPPSIKANGKDDH			
rACNG	(51)	ETRRRAQTPESTGHTWRMTEKSNGVKSSPANNHNHHVPAIKANGKDDHES			
			101		150
HBMYCNG	(33)	RASSRPHSAADDTSSELQRЛАMDAPQOGRSGFRRIVRLVGIIRFWAN			
CNG2_BOS	(33)	RASSRPQSAADDTSSELQLAEMDAPQQRGGFRRIVRLVGIIRFWAY			
CNG2_MOUSE	(34)	RAGSRPQSVADDTSSELQRЛАEMDTPRRGRRGGFRRIVRLVGIIRDWAN			
CNG2_RAT	(34)	RAGSRPQSVADDTSSELQRЛАEMDTPRRGRRGGFRRIVRLVGVIRDWAN			
rACNG	(101)	RTRSRPQSAADDTSSELQRЛАEMDAPQQRGGFRRIVRLVGVIRWAN			
			151		200
HBMYCNG	(82)	KNFREEEPRPDSFLERFRGPELQTVTTQEGDGKGDKDGEDKGTKKKFELF			
CNG2_BOS	(82)	RNFREEEPRPDSFLERFRGPELHTVTTQGDGKGDKDGEKGKGTKKKFELF			
CNG2_MOUSE	(84)	KNFREEEPRPDSFLERFRGPELQTVTHQGDGKGDKDGEKGKGTKKKFELF			
CNG2_RAT	(84)	KNFREEEPRPDSFLERFRGPELQTVTHQGDGKGDKDGEKGKGTKKKFELF			
rACNG	(150)	RNFREEEARPDSFLERFRGPELQTVTTOQGDGKGDKDGDGKGKGTKKKFELF			
			201		250
HBMYCNG	(132)	VLDPAGDLYCWLFIAMPVLYNWCLLVARACFSDLQKGYYIVWLVDYV			
CNG2_BOS	(132)	VLDPAGDWYYRWLFIAFPVLYNWCLLVARACFSDLQKGYYIVWLVDYV			
CNG2_MOUSE	(134)	VLDPAGDWYYRWLFVIAAMPVLYNWCLLVARACFSDLQRNYFVWLVDYF			
CNG2_RAT	(134)	VLDPAGDWYYRWLFVIAAMPVLYNWCLLVARACFSDLQRNYFVWLVDYF			
rACNG	(200)	VLDPAGDWYYRWLFVIAAMPVLYNWCLLVARACFSDLQRGYFVWLVDYF			
			251		300
HBMYCNG	(182)	SDVYYIADLFIRLRTGFLEQGLLVKDKKLRDNYIHTLQFKLDVASIIP			
CNG2_BOS	(182)	SDVYYIADLFIRLRTGFLEQGLLVKDKKLRDNYIHTMOKLVDVASIIP			
CNG2_MOUSE	(184)	SDVYYIADLFIRLRTGFLEQGLLVKDPKKKLRDNYIHTLQFKLDVASIIP			
CNG2_RAT	(184)	SDVYYIADLFIRLRTGFLEQGLLVKDPKKKLRDNYIHTLQFKLDVASIIP			
rACNG	(250)	SDVYYIADLFIRLRTGFLEQGLLVKDPKKKLRDNYIHTLQFKLDVASIIP			
			301		350
HBMYCNG	(232)	DLIYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTYPNIFRISNLVLY			
CNG2_BOS	(232)	DLIYFAVGIIHNPPEVRFNRLLHFARMFEFFDRTETRTYPNIFRISNLVLY			
CNG2_MOUSE	(234)	DLIYFAVGIIHSPEVRFNRLLHFARMFEFFDRTETRTYPNIFRISNLVLY			
CNG2_RAT	(234)	DLIYFAVGIIHSPEVRFNRLLHFARMFEFFDRTETRTYPNIFRISNLVLY			
rACNG	(300)	DLIYFAVGIIHNPETRFNRLLHFARMFEFFDRTETRTYPNIFRISNLVLY			
			351		400
HBMYCNG	(282)	ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS			
CNG2_BOS	(282)	ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS			
CNG2_MOUSE	(284)	ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS			
CNG2_RAT	(284)	ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS			
rACNG	(350)	ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS			

FIG. 4 (Continued)

				450
HBMYCNG	(332)	401	TLTLTTIGETPPPVKDEEYLVIFDFLIGVLIFATIVGNVGSMSISNNNAT	
CNG2_BOS	(332)		TLTLTTIGETPPPVKDEEYLVIFDFLIGVLIFATIVGNVGSMSISNNNAT	
CNG2_MOUSE	(334)		TLTLTTIGETPPPVKDEEYLFFIFDFLIGVLIFATIVGNVGSMSISNNNAT	
CNG2_RAT	(334)		TLTLTTIGETPPPVKDEEYLVIFDFLIGVLIFATIVGNVGSMSISNNNAT	
rACNG	(400)		TLTLTTIGETPPPVKDEEYLVIFDFLIGVLIFATIVGNVGSMSISNNNAT	
				500
HBMYCNG	(382)	451	RAEFQAKIDAVKHMYQFRKVSKEMEAKVIRWFDYLWTNKKTVDEREVLK	
CNG2_BOS	(382)		RAEFQAKIDAVKHMYQFRKVSKEMEAKVIRWFDYLWTNKKSVDEREVLK	
CNG2_MOUSE	(384)		RAEFQAKIDAVKHMYQFRKVSKEMEAKVIRWFDYLWTNKKTVDEREVLK	
CNG2_RAT	(384)		RAEFQAKIDAVKHMYQFRKVSKEMEAKVIRWFDYLWTNKKTVDEREVLK	
rACNG	(450)		RAEFQAKIDAVKHMYQFRKVSKEMEAKVIRWFDYLWTNKKTVDEREVLK	
				550
HBMYCNG	(432)	501	LPAKLRAEIAINVHLSTLKKVRIFFDCEAGILLVELVLKLRPQVFSPGDYI	
CNG2_BOS	(432)		LPAKLRAEIAINVHLSTLKKVRIFFDCEAGILLVELVLKLRPQVFSPGDYI	
CNG2_MOUSE	(434)		LPAKLRAEIAINVHLSTLKKVRIFFDCEAGILLVELVLKLRPQVFSPGDYI	
CNG2_RAT	(434)		LPAKLRAEIAINVHLSTLKKVRIFFDCEAGILLVELVLKLRPQVFSPGDYI	
rACNG	(500)		LPAKLRAEIAINVHLSTLKKVRIFFDCEAGILLVELVLKLRPQVFSPGDYI	
				600
HBMYCNG	(482)	551	CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
CNG2_BOS	(482)		CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
CNG2_MOUSE	(484)		CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
CNG2_RAT	(484)		CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
rACNG	(550)		CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK	
				650
HBMYCNG	(532)	601	MGNRTTANIRSLGYSDFCLSKDDLMEAVTEYPDAAKVLLEERGREILMKE	
CNG2_BOS	(532)		MGNRTTANIRSLGYSDFCLSKDDLMEAVTEYPDAAKVLLEERGREILMKE	
CNG2_MOUSE	(534)		MGNRTTANIRSLGYSDFCLSKDDLMEAVTEYPDAAKVLLEERGREILMKE	
CNG2_RAT	(534)		MGNRTTANIRSLGYSDFCLSKDDLMEAVTEYPDAAKVLLEERGREILMKE	
rACNG	(600)		MGNRTTANIRSLGYSDFCLSKDDLMEAVTEYPDAAKVLLEERGREILMKE	
				700
HBMYCNG	(582)	651	GLLDENEVAASMEVDVQEKLQLETNMELTYTRFGRLLAEYTGAQQKLKQ	
CNG2_BOS	(582)		GLLDENEVAASMEVDVQEKLQLETNMELTYTRFGRLLAEYTGAQQKLKQ	
CNG2_MOUSE	(584)		GLLDENEVAASMEVDVQEKLQLETNMELTYTRFGRLLAEYTGAQQKLKQ	
CNG2_RAT	(584)		GLLDENEVAASMEVDVQEKLQLETNMELTYTRFGRLLAEYTGAQQKLKQ	
rACNG	(650)		GLLDENEVAASMEVDVQEKLQLETNMELTYTRFGRLLAEYTGAQQKLKQ	
				733
HBMYCNG	(632)	701	RITVLETKMKQNNEDDYLSDGMSPELAAADEP	
CNG2_BOS	(632)		RITVLETKMKQNNEDDYLSDGMSPEPAAEKP-	
CNG2_MOUSE	(634)		RITVLETKMKQNHEDDYLSDGINTPEPAAE--	
CNG2_RAT	(634)		RITVLETKMKQNHEDDYLSDGINTPEPAAE--	
rACNG	(700)		RITVLETKMKQNTEDDYLSDGMSPEPAAAEQP	

FIG. 5

1 CTCTAGATGTACATGGAGGATGACCGAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA 60
 1 M T E K T N G V K S S P A N 14
 61 TAATCACAAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCACAGGAC 120
 15 N H N H H A P P A I K A N G K D D H R T 34
 121 AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC 180
 35 S S R P H S A A D D D T S S E L Q R L A 54
 181 AGACGTGGATGCCACAGCAGGGAGGAGTGGCTTCCGCAGGATAGTTGCCTGGTGGG 240
 55 D V D A P Q Q G R S G F R R I V R L V G 74
 241 GATCATCAGAGAATGGCCAACAAGAATTCCAGAGGAGGAACTAGGCCTGACTCATT 300
 75 I I R E W A N K N F R E E E P R P D S F 94
 301 CCTCGAGCGTTTCGTGGCCTGAACCTCCAGACTGTGACCACACAGGAGGGATGGCAA 360
 95 L E R F R G P E L Q T V T T Q E G D G K 114
 361 AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTGAACTATTTGTCTTGG 420
 115 G D K D G E D K G T K K K F E L F V L D 134
 421 CCCAGCTGGGATTTGTACTACTGCTGGTATTGTCAATTGCCATGCCGTCTTACAA 480
 135 P A G D L Y Y C W L F V I A M P V L Y N 154
 481 CTGGTGCCTGCTGGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT 540
 155 W C L L V A R A C F S D L Q K G Y Y L V 174
 541 GTGGCTGGCTGGATTATGTCTCAGATGTGGTCTACATTGGACCTCTTCATCCGATT 600
 175 W L V L D Y V S D V V Y I A D L F I R L 194
 601 GCGCACAGGTTCTGGAGCAGGGCTGCTGGCAAAAGATAACCAAGAACTGCGAGACAA 660
 195 R T G F L E Q G L L V K D T K K L R D N 214
 661 CTACATCCACACCCCTGCAGTTCAAGCTGGATGTGGCTTCCATCCCCACTGACCTGAT 720
 215 Y I H T L Q F K L D V A S I I P T D L I 234
 721 CTATTTGCTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCCTGCTGCACCTTG 780
 235 Y F A V D I H S P E V R F N R L L H F A 254
 781 CCGCATGTTGAGTTCTTGACCGGACAGAGACACGCACCAACTACCCCTAACATCTTCCG 840
 255 R M F E F F D R T E T R T N Y P N I F R 274
 841 CATCAGCAACCTGCTCTACATCTGGTCATCATCCACTGGAATGCCTGCATCTATT 900
 275 I S N L V L Y I L V I I H W N A C I Y Y 294
 901 TGCCATCTCAAATCCATAGGCTTGGGTCGACACCTGGTTACCCAAACATCACTGA 960
 295 A I S K S I G F G V D T W V Y P N I T D 314

FIG. 5 (Cont'd)

961	CCCTGAGTATGGCTACCTGGCTAGGGAAATACATCTATTGCCCTTACTGGTCCACACTGAC	1020
315	P E Y G Y L A R E Y I Y C L Y W S T L T	334
1021	TCTCACTACCATTGGGGAGACACCACCCCTGTAAAGGATGAGGGAGTACCTATTTGTCAT	1080
335	L T T I G E T P P P V K D E E Y L F V I	354
1081	CTTGACTTCCTGATTGGCGTCCTCATCTTGCCACCATCGTGGAAATGTGGGCTCCAT	1140
355	F D F L I G V L I F A T I V G N V G S M	374
1141	GATCTCCAACATGAATGCCACCCGGGAGAGTCCAGGCTAACATCGATGCCGTGAAACA	1200
375	I S N M N A T R A E F Q A K I D A V K H	394
1201	CTACATGCAGTTCGAAAGGTCAAGCAAGGGATGGAAGCCAAGCTCATTAGGTGGTTGA	1260
395	Y M Q F R K V S K G M E A K V I R W F D	414
1261	CTACTTGTGGACCAATAAGAACAGACTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC	1320
415	Y L W T N K K T V D E R E I L K N L P A	434
1321	CAAGCTCAGGGCTGAGATAGCCATCAATGTCCACTTGTCCACACTCAAGAAAGTGCAGC	1380
435	K L R A E I A I N V H L S T L K K V R I	454
1381	CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCTCAGGT	1440
455	F H D C E A G L L V E L V L K L R P Q V	474
1441	CTTCAGTCTGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT	1500
475	F S P G D Y I C R K G D I G K E M Y I I	494
1501	TAAGGAGGGCAAACCTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTCTGCTGTC	1560
495	K E G K L A V V A D D G V T Q Y A L L S	514
1561	GGCTGGAAGCTGCTTGGCGAGATCAGTATCCTAACATTAAGGGCAGTAAATGGCAA	1620
515	A G S C F G E I S I L N I K G S K M G N	534
1621	TCGACGCACAGCTAATATCCGCAGCCTGGCTACTCAGATCTCTCTGCTTGTCCAAGGA	1680
535	R R T A N I R S L G Y S D L F C L S K D	554
1681	TGATCTTATGGAAGCTGTGACTGAGTACCCCTGATGCCAAGAAAGTCCTAGAAGAGAGGG	1740
555	D L M E A V T E Y P D A K K V L E E R G	574
1741	TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAACGAAAGTGGCAACCAGCATGGA	1800
575	R E I L M K E G L L D E N E V A T S M E	594
1801	GGTCGACGTGCAGGAGAACGCTAGGGCAGCTGGAGACCAACATGGAAACCTTGTACACTCG	1860
595	V D V Q E K L G Q L E T N M E T L Y T R	614
1861	CTTTGGCGCCTGCTGGCTGAGTACACGGGGCCAGCAGAACGCTCAAGCAGCGCATCAC	1920
615	F G R L L A E Y T G A Q Q K L K Q R I T	634

FIG. 5 (Cont'd)

1921	AGTTCTGGAAACCAAGATGAAACAGAACAAATGAAGATGACTACCTGTCTGATGGGATGAA	1980
635	V L E T K M K Q N N E D D Y L S D G M N	654
1981	CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGCCAACTGCCTCTCCAG	2040
655	S P E L A A A D E P	664
2041	CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTAGATCTCCGGATTTACAT	2100
2101	GCATTACCCCTCATGTTCCCTGAATTCTCCAAAAGCCTCTGACCTGGGTTTGGCC	2160
2161	TAAACATCCAAGATTCCGCCTCGGATCCCG	2190

FIG. 6

MTEKTNGVKSSPANNHHAPPAIKANGKDDHRTSSRPHSAADDTSSELQRLADVDAPQQGRSGFRRI
VRLVGIIREWANKNFREEEPRPDSFLERFRGFELQTTQEGDGKGDKGEDGKGTKKFELFVLDPA
LYCWLFIAMPVLYNWCLLVARACFSQDLQKGYYLVLVLDYVSDVVIADLFIRLRTGFLEQGLLV
TKKLRDNYIHTLQFKLDVASIIPDLYFAVDIHSPEVRFNRLHFARMFEFFDRTETRTNYPNIFRIS
NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLT
KDEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKGMEAKVIRW
YLWTNKKTVDEREILKNLPAKLRAEIAINVLSTLKKVRIHDCEAGLLVELVLRPQVFSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTVQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYS
KDDLMEEAVTEYPDACKVLEERGREILMKEGLLDENEVATSMEVDVQEKLGOLETNMETLYTRFG
YTGAQQQLKQORITVLETKMKQNNEDDYLSDGMSPELAADEP

FIG. 7

1 MTEKTNGVKSSPANNHNHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50
 |||||||
 1 MTEKTNGVKSSPANNHNHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50
 |||||||
 51 QRLADVDAPQQGRSGFRRIVRLVGIREWANKNFREEEPRPDSFLERFRG 100
 |||||||
 51 QRLADVDAPQQGRSGFRRIVRLVGIREWANKNFREEEPRPDSFLERFRG 100
 |||||||
 101 PELQTVTQEGDGKGDKGDKGEDKGTKKFELFVLDPAGDLYYCWLFIAMP 150
 |||||||
 101 PELQTVTQEGDGKGDKGDKGEDKGTKKFELFVLDPAGDLYYCWLFIAMP 150
 |||||||
 151 VLYNWCLLVARACFSDLQKGYYLVWLVLVDYVSDVVIADLFIRLRTGFLE 200
 |||||||
 151 VLYNWCLLVARACFSDLQKGYYLVWLVLVDYVSDVVIADLFIRLRTGFLE 200
 |||||||
 201 QGLLVKDTKLLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRL 250
 |||||||
 201 QGLLVKDTKLLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRL 250
 |||||||
 251 LHFARMFEFFDRTETRTNYPNIFRISNLVLYILVIHWNACIYYAISKSI 300
 |||||||
 251 LHFARMFEFFDRTETRTNYPNIFRISNLVLYILVIHWNACIYYAISKSI 300
 |||||||
 301 GFGVDTWVYPNITDPEYGYLAREYIYCLWSTLTTLTIGETPPPVKDEEY 350
 |||||||
 301 GFGVDTWVYPNITDPEYGYLAREYIYCLWSTLTTLTIGETPPPVKDEEY 350
 |||||||
 351 LFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHMQFRK 400
 |||||||
 351 LFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHMQFRK 400
 |||||||
 401 VSKGMEAKVIRWFDYLWTNKKTVDEREILKNLPAKLRAEIAINVHLSTLK 450
 |||||||
 401 VSKGMEAKVIRWFDYLWTNKKTVDEREILKNLPAKLRAEIATNVHLSTLK 450
 |||||||
 451 KVRIFHDCEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLA 500
 |||||||
 451 KVRIFHDCEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLA 500
 |||||||
 501 VVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRTANIRSLGYSDFC 550
 |||||||
 501 VVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRTANIRSLGYSDFC 550
 |||||||
 551 LSKDDLMEAVENTEYPAKKVLEERGREILMKEGLLDENEVATSMEVDVQEK 600
 |||||||
 551 LSKDDLMEAVENTEYPAKKVLEERGREILMKEGLLDENEVATSMEVDVQEK 600
 |||||||
 601 LGQLETNMETLYTRFGRLLAEYTGAQQKLKQRITVLETKMKQNNEDDYL 650
 |||||||
 601 LGQLETNMETLYTRFGRLLAEYTGAQQKLKQRITVLETKMKQNNEDDYL 650
 |||||||
 651 DGMNSPELAAADEP* 665
 |||||||
 651 DGMNSPELAAADEP. 664